Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method for amplifying a nucleic acid sample from blood comprising:

providing a nucleic acid sample from blood;

hybridizing at least one reduction oligonucleotide to at least one globin mRNA ~~unwanted RNA~~ in the sample;

incubating the mixture with an RNase H and subsequently inactivating the RNase H;

hybridizing a primer comprising oligo dT and an RNA polymerase promoter sequence to the RNA in the mixture;

extending the primer to make single-stranded cDNA; making double-stranded cDNA comprising a functional RNA polymerase promoter from said single-stranded cDNA; and

synthesizing multiple copies of labeled RNA from the double stranded cDNA using an RNA polymerase ~~amplifying the cDNA~~.

2. (currently amended) The method of claim 1 wherein the globin mRNA ~~unwanted RNA~~ comprises a poly(A) tail and wherein the reduction oligonucleotide hybridizes to the globin mRNA ~~unwanted RNA~~ in the region of the globin mRNA ~~unwanted RNA~~ that is near the 5' end of the poly(A) tail of the globin mRNA ~~unwanted RNA~~.

3. (original) The method of claim 1 wherein the RNase H is inactivated by depleting RNase H from the mixture.

4. (original) The method of claim 1 wherein the RNase H is thermolabile and inactivation is by heating.

5. (original) The method of claim 1 wherein the RNase H is inactivated by addition of EDTA to the mixture.

6. (original) The method of claim 1 wherein the RNase H is inactivated by separating the RNase H from the nucleic acid by organic extraction.

7. (original) The method of claim 1 wherein the RNase H is removed by separating the RNA from the RNase H by column purification.

8. (canceled)

9. (canceled)

10. (canceled)

11. (currently amended) The method of claim 1 wherein the globin mRNA ~~unwanted nucleic acid~~ is selected from the group consisting of alpha-1 globin, alpha-2 globin and beta globin.

12. (currently amended) The method of claim [~~10~~] 1 wherein a plurality of different species of reduction oligonucleotides are used and each species is complementary to a different globin mRNA.

13. (currently amended) The method of claim 1 wherein after hybridizing the reduction oligonucleotide to the ~~unwanted~~ globin mRNA, the reduction oligonucleotide is extended by a polymerase.

14. (original) The method of claim 1 wherein after incubating the mixture with RNase H the reduction oligonucleotide is removed.

15. (original) The method of claim 1 wherein the at least one reduction oligonucleotide consists essentially of SEQ ID NO 1.

16. (original) The method of claim 1 wherein the at least one reduction oligonucleotide consists essentially of SEQ ID NO 2.

17. (original) The method of claim 1 wherein the at least one reduction oligonucleotide consists essentially of SEQ ID NO 3.

18. (original) The method of claim 1 wherein a mixture of different sequence reduction oligonucleotides are added to the mixture.

19. (currently amended) The method of claim 18 wherein the mixture of different sequence reduction oligonucleotides comprises an oligonucleotide consisting of SEQ ID NO 1, an oligonucleotide consisting of SEQ ID NO 2 and an oligonucleotide consisting of SEQ ID NO 3 ~~SEQ ID NOs 1, 2 and 3~~.

20. (original) The method of claim 1 wherein said nucleic acid sample from blood is obtained from blood that was collected in a container containing an RNA stabilizing agent.

21. (original) The method of claim 20 wherein said RNA stabilizing agent is selected from the group consisting of cationic compounds, detergents, chaotropic salts, ribonuclease inhibitors, chelating agents, and mixtures thereof.

22. (original) The method of claim 20 wherein said RNA stabilizing agent is selected from the group consisting of phenol, chloroform, acetone, alcohols and mixtures thereof.

23. (original) The method of claim 20 wherein said nucleic acid sample from blood is obtained from blood that was collected in a container containing a RNA stabilizing agent and wherein said RNA stabilizing agent is selected from the group consisting of mercapto-alcohols, di-thio-threitol (DTT), and mixtures thereof.

24. (Previously presented) A method for analyzing a nucleic acid sample isolated from blood comprising:

a. providing a first nucleic acid sample obtained from a blood sample;
b. blocking amplification of globin mRNA sequences in the nucleic acid sample by hybridizing a reduction oligonucleotide to said globin mRNA sequences to form a RNA:DNA hybrid and digesting the RNA:DNA hybrid;
c. amplifying unblocked nucleic acid sequences to produce an amplified nucleic acid sample;
d. contacting said amplified nucleic acid sample with a solid support comprising nucleic acid probes to generate a hybridization pattern; and
e. analyzing the hybridization pattern.

25. (original) The method of claim 24, further comprising: detecting the presence or absence of hybridization of said amplified nucleic acid sample to said nucleic acid probes on said solid support.

26. (original) The method of claim 24, further comprising: labeling said amplified nucleic acid sample.

27. (canceled)

28. (original) The method of claim 24 wherein said unblocked nucleic acid sequences are non-specifically amplified by in vitro transcription.

29. (canceled)

30. (Previously presented) The method of claim 24 wherein said globin mRNAs are greater than 20% of the first nucleic acid sample and wherein said globin mRNAs are less than 20% of the amplified nucleic acid sample.

31. (currently amended) A method for ~~amplifying~~ analyzing a nucleic acid sample from blood comprising:

providing a nucleic acid sample from blood;

hybridizing at least one reduction oligonucleotide to at least one globin mRNA in the sample generating reduction oligonucleotide: globin mRNA complexes;

removing said complexes from the sample; [~~and,~~]

amplifying at least one target RNA remaining in the sample by a method comprising adding random primers to the sample, extending the random primers to make cDNA and labeling the cDNA; and,

hybridizing the labeled cDNA to an array of nucleic acid probes and analyzing a resulting hybridization pattern.

32. (Previously presented) The method of claim 31 wherein said complexes are removed from the sample by affinity purification.

33. (Previously presented) The method of claim 31 wherein said reduction oligonucleotide comprises biotin and said complexes are removed from the sample by hybridization to a solid support.

34. (original) The method of claim 33 wherein said solid support comprises streptavidin.

35. (canceled)

36. (canceled)

37. (Previously presented) A method of analyzing a nucleic acid sample from a blood sample comprising:

amplifying mRNA from the nucleic acid sample to generate an amplified sample wherein amplification of globin mRNA is blocked during said amplifying step;

labeling said amplified sample;

hybridizing the amplified sample to an array of nucleic acid probes to generate a hybridization pattern; and

analyzing the hybridization pattern.

38. (Previously presented) The method of claim 37 wherein said amplifying step comprises hybridizing an extendable primer comprising oligo dT to said nucleic acid sample, extending said primer with a reverse transcriptase to make cDNA and amplifying said cDNA.

39. (Previously presented) The method of claim 38 wherein amplification of globin mRNA is blocked by hybridization of one or more blocking molecules to one or more globin mRNA transcripts prior to extending said extendable primer with reverse transcriptase, wherein said one or more blocking molecules hybridize to said one or more

globin mRNA transcripts and block reverse transcription of said globin mRNA transcripts.

40. (Currently amended) The method of claim [~~38~~] 39 wherein said one or more blocking molecules are peptide nucleic acids.

41. (Previously presented) The method of claim 39 wherein said one or more blocking molecules hybridize to a globin mRNA selected from the group consisting of alpha-1 globin, alpha-2 globin and beta globin.

42. (Previously presented) The method of claim 37 wherein the hybridization pattern is analyzed to determine an expression profile for said nucleic acid sample.

43. (Previously presented) The method of claim 37 wherein said nucleic acid sample is isolated from a blood sample that was collected in a container containing an RNA stabilizing agent selected from the group consisting of cationic compounds, detergents, chaotropic salts, ribonuclease inhibitors, chelating agents, phenol, chloroform, acetone, alcohols, mercapto-alcohols, di-thio-threitol (DTT), and mixtures thereof.

44. (new) The method of claim 24 wherein the reduction oligonucleotide is selected from the group consisting of an oligonucleotide consisting of SEQ ID NO 1, an oligonucleotide consisting of SEQ ID NO 2 and an oligonucleotide consisting of SEQ ID NO 3.

45. (new) The method of claim 24 wherein a mixture of reduction oligonucleotides is added in step b. wherein the mixture comprises an oligonucleotide consisting of SEQ ID NO 1, an oligonucleotide consisting of SEQ ID NO 2 and an oligonucleotide consisting of SEQ ID NO 3.